

## **AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently Amended) A compound comprising two or more antigen binding regions linked to at least one prodrug-activating enzyme, wherein
  - a) the antigen binding regions consist of a single polypeptide chain;
  - b) the single polypeptide chain is comprised of a first variable domain, a second variable domain, and a polypeptide linker connecting the first variable domain and the second variable domain, wherein a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that links the first variable domain and the second variable domain; ~~and~~ wherein
  - c) the compound has a bivalent or a multivalent structure; and wherein
  - d) the compound is glycosylated.
2. (Previously Presented) A compound as claimed in claim 1, wherein the compound further comprises covalently bonded carbohydrates.
3. (Previously Presented) A compound as claimed in claim 1, wherein at least one antigen binding region comprises a variable domain of a heavy antibody chain and a variable domain of a light antibody chain (sFv fragment).
4. (Original) A compound as claimed in claim 1, wherein the antigen binding region binds to a tumor-associated antigen (TAA).

5. (Previously Presented) A compound as claimed in claim 4, wherein the TAA is selected from the group consisting of an N-CAM, PEM, EGF-R, Sialyl-Le<sup>a</sup>, Sialyl-Le<sup>x</sup>, TF $\beta$ , GICA, GD<sub>3</sub>, GD<sub>2</sub>, TAG72, CA125, the 24-25 kDa glycoprotein defined by Mab L6, and CEA.

6. (Previously Presented) A compound as claimed in claim 1, wherein the enzyme is selected from the group consisting of a lactamase, pyroglutamate aminopeptidase, D-aminopeptidase, oxidase, peroxidase, phosphatase, hydroxynitrile lyase, protease, esterase, carboxypeptidase and glycosidase.

7. (Previously Presented) A compound as claimed in claim 6, wherein the enzyme is a  $\beta$ -glucuronidase, which is selected from the group consisting of an *E. coli*  $\beta$ -glucuronidase, a *Kobayasia nipponica*  $\beta$ -glucuronidase, a *Secale cereale*  $\beta$ -glucuronidase and a human  $\beta$ -glucuronidase.

8. (Original) A compound as claimed in claim 1, wherein the antigen binding region is linked to the enzyme via a peptide linker.

9. (Previously Presented) A compound as claimed in claim 2, wherein glycosylation covalently bonds the carbohydrates to the compound, and the glycosylation takes place either by means of chemical methods or by a selection of suitable expression systems.

10. (Previously Presented) A compound as claimed in claim 1, which has undergone secretory expression in *Saccharomyces cerevisiae* or in *Hansenula polymorpha*.

11. (Previously Presented) A compound as claimed in claim 1, which is expressed in *E. coli* and is subsequently chemically glycosylated.

12. (Currently Amended) A compound as claimed in claim 30, wherein the sFv- $\beta$ -lactamase fusion protein has undergone periplasmic expression in *E. coli* and is subsequently chemically glycosylated.

13. (Previously Presented) A compound as claimed in claim 30, wherein the sFv- $\beta$ -lactamase fusion protein has undergone secretory expression in *Saccharomyces cerevisiae* or *Hansenula polymorpha*.

14. (Withdrawn) A nucleic acid coding for a compound as claimed in claim 1.

15. (Withdrawn) A nucleic acid as claimed in claim 14, coding for a humanized sFv fragment against CEA and a human  $\beta$ -glucuronidase.

16. (Withdrawn) A nucleic acid as claimed in claim 14 with the sequence

CCAAGCTTAT GAATATGCAA ATCCTGCTCA TGAATATGCA AATCCTCTGA	50
ATCTACATGG TAAATATAGG TTTGTCTATA CCACAAACAG AAAAACATGA	100
GATCACAGTT CTCTCTACAG TTAGTGAGCA CACAGGACCT CACC ATG GGA TGG	153
AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGTAAGGGGC	199
Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr	
-10	
TCACAGTAGC AGGCTTGAGG TCTGGACATA TATATGGGTG ACAATAGACAT	249
CCACTTTGCC TTTCTCTCCA CA GGT GTC CAC TCC CAG GTC CAA CTG CAG	298
Gly Val His Ser Gln Val Gln Leu Gln	
1	
GAG AGC GGT CCA GGT CTT GTG AGA CCT AGC CAG ACC CTG AGC CTG	343
Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln Thr Leu Ser Leu	
10	
ACC TGC ACC GTG TCT GGC TTC ACC ATC AGC AGT GGT TAT AGC TGG	388
Thr Cys Thr Val Ser Gly Phe Thr Ile Ser Ser Gly Tyr Ser Trp	
30	
CAC TGG GTG AGA CAG CCA CCT GGA CGA GGT CTT GAG TGG ATT GGA	433
His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly	
40	
TAC ATA CAG TAC AGT GGT ATC ACT AAC TAC AAC CCC TCT CTC AAA	478
Tyr Ile Gln Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys	
60	
AGT AGA GTG ACA ATG CTG GTA GAC ACC AGC AAG AAC CAG TTC AGC	523

Ser Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser  
 70 80  
 CTG AGA CTC AGC AGC GTG ACA GCC GCC GAC ACC GCG GTC TAT TAT 568  
 Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr  
 90  
 TGT GCA AGA GAA GAC TAT GAT TAC CAC TGG TAC TTC GAT GTC TGG 613  
 Cys Ala Arg Glu Asp Tyr Asp Tyr His Trp Tyr Phe Asp Val Trp  
 100 110  
 GGC CAA CCC ACC ACG GTC ACC GTC TCC TCA GGA GGC GGT GGA TCG 658  
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser  
 120  
 GGC GGT GGT GGG TCG GGT GGC GGC GGA TCT GAC ATC CAG CTG ACC 703  
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu Thr  
 130 140  
 CAG AGC CCA AGC AGC CTG AGC GCC AGC CTC GGT GAC AGA GTG ACC 748  
 Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr  
 150  
 ATC ACC TGT AGT ACC AGC TCG AGT GTA AGT TAC ATG CAC TGG TAC 793  
 Ile Thr Cys Ser Thr Ser Ser Ser Val Ser Tyr Met His Trp Tyr  
 160 170  
 CAG CAG AAG CCA GGT AAG GCT CCA AAG CTG CTG ATC TAC AGC ACA 838  
 Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Thr  
 180  
 TCC AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT 883  
 Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly  
 190 200  
 AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG 928  
 Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu  
 210  
 GAC ATC GCC ACC TAC TAC TGC CAT CAG TGG AGT AGT TAT CCC ACG 973  
 Asp Ile Ala Thr Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Thr  
 220 230  
 TTC GGC CAA GGG ACC AAG CTG GAG ATC AAA GGTGAGTAGA ATTTAACTTT 1023  
 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
 240  
 TGCTTCCTCA GTTGGATCTG AGTAACTCCC AATCTTCTCT CTGCA GAG CTC AAA 1077  
 Glu Leu Lys  
 ACC CCA CTT GGT GAC ACA ACT CAC ACA TGC CCA CGG TGC CCA 1119  
 Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro Arg Cys Pro  
 250  
 GGTAAGCCAG CCCAGGACTC GCCCTCCAGC TCAAGGCGGG ACAAGAGCCC 1169  
 TAGAGTGGCC TGAGTCCAGG GACAGGCCC AGCAGGGTGC TGACGCATCC 1219  
 ACCTCCATCC CAGATCCCCG TAACTCCCAA TCTTCTCTCT GCA GCG GCG GCG 1271  
 Ala Ala Ala  
 260  
 GCG GTG CAG GGC GGG ATG CTG TAC CCC CAG GAG AGC CCG TCG CGG 1316  
 Ala Val Gln Gly Gly Met Leu Tyr Pro Gln Glu Ser Pro Ser Arg  
 270  
 GAG TGC AAG GAG CTG GAC GGC CTC TGG AGC TTC CGC GCC GAC TTC 1361

Glu Cys Lys Glu Leu Asp Gly Leu Trp Ser Phe Arg Ala Asp Phe	
280 290	
TCT GAC AAC CGA CGC CGG GGC TTC GAG GAG CAG TGG TAC CGG CGG	1406
Ser Asp Asn Arg Arg Arg Gly Phe Glu Glu Gln Trp Tyr Arg Arg	
300	
CCG CTG TGG GAG TCA GGC CCC ACC GTG GAC ATG CCA GTT CCC TCC	1451
Pro Leu Trp Glu Ser Gly Pro Thr Val Asp Met Pro Val Pro Ser	
310 320	
AGC TTC AAT GAC ATC AGC CAG GAC TGG CGT CTG CGG CAT TTT GTC	1496
Ser Phe Asn Asp Ile Ser Gln Asp Trp Arg Leu Arg His Phe Val	
330	
GGC TGG GTG TGG TAC GAA CGG GAG GTG ATC CTG CCG GAG CGA TGG	1541
Gly Trp Val Trp Tyr Glu Arg Glu Val Ile Leu Pro Glu Arg Trp	
340 350	
ACC CAG GAC CTG CGC ACA AGA GTG GTG CTG AGG ATT GGC AGT GCC	1586
Thr Gln Asp Leu Arg Thr Arg Val Val Leu Arg Ile Gly Ser Ala	
360	
CAT TCC TAT GCC ATC GTG TGG GTG AAT GGG GTC GAC ACG CTA GAG	1631
His Ser Tyr Ala Ile Val Trp Val Asn Gly Val Asp Thr Leu Glu	
370 380	
CAT GAG GGG GGC TAC CTC CCC TTC GAG GCC GAC ATC AGC AAC CTG	1676
His Glu Gly Gly Tyr Leu Pro Phe Glu Ala Asp Ile Ser Asn Leu	
390	
GTC CAG GTG GGG CCC CTG CCC TCC CGG CTC CGA ATC ACT ATC GCC	1721
Val Gln Val Gly Pro Leu Pro Ser Arg Leu Arg Ile Thr Ile Ala	
400 410	
ATC AAC AAC ACA CTC ACC CCC ACC ACC CTG CCA CCA GGG ACC ATC	1766
Ile Asn Asn Thr Leu Thr Pro Thr Thr Leu Pro Pro Gly Thr Ile	
420	
CAA TAC CTG ACT GAC ACC TCC AAG TAT CCC AAG GGT TAC TTT GTC	1811
Gln Tyr Leu Thr Asp Thr Ser Lys Tyr Pro Lys Gly Tyr Phe Val	
430 440	
CAG AAC ACA TAT TTT GAC TTT TTC AAC TAC GCT GGA CTG CAG CGG	1856
Gln Asn Thr Tyr Phe Asp Phe Phe Asn Tyr Ala Gly Leu Gln Arg	
450	
TCT GTA CTT CTG TAC ACG ACA CCC ACC ACC TAC ATC GAT GAC ATC	1901
Ser Val Leu Leu Tyr Thr Thr Pro Thr Thr Tyr Ile Asp Asp Ile	
460 470	
ACC GTC ACC ACC AGC GTG GAG CAA GAC AGT GGG CTG GTG AAT TAC	1946
Thr Val Thr Thr Ser Val Glu Gln Asp Ser Gly Leu Val Asn Tyr	
480	
CAG ATC TCT GTC AAG GGC AGT AAC CTG TTC AAG TTG GAA GTG CGT	1991
Gln Ile Ser Val Lys Gly Ser Asn Leu Phe Lys Leu Glu Val Arg	
490 500	
CTT TTG GAT GCA GAA AAC AAA GTC GTG GCG AAT GGG ACT GGG ACC	2036
Leu Leu Asp Ala Glu Asn Lys Val Val Ala Asn Gly Thr Gly Thr	
510	
CAG GGC CAA CTT AAG GTG CCA GGT GTC AGC CTC TGG TGG CCG TAC	2081
Gln Gly Gln Leu Lys Val Pro Gly Val Ser Leu Trp Trp Pro Tyr	
520 530	
CTG ATG CAC GAA CGC CCT GCC TAT CTG TAT TCA TTG GAG GTG CAG	2126

Leu Met His Glu Arg Pro Ala Tyr Leu Tyr Ser Leu Glu Val Gln	
540	
CTG ACT GCA CAG ACG TCA CTG GGG CCT GTG TCT GAC TTC TAC ACA	2171
Leu Thr Ala Gln Thr Ser Leu Gly Pro Val Ser Asp Phe Tyr Thr	
550 560	
CTC CCT GTG GGG ATC CGC ACT GTG GCT GTC ACC AAG AGC CAG TTC	2216
Leu Pro Val Gly Ile Arg Thr Val Ala Val Thr Lys Ser Gln Phe	
570	
CTC ATC AAT GGG AAA CCT TTC TAT TTC CAC GGT GTC AAC AAG CAT	2261
Leu Ile Asn Gly Lys Pro Phe Tyr Phe His Gly Val Asn Lys His	
580 590	
GAG GAT GCG GAC ATC CGA GGG AAG GGC TTC GAC TGG CCG CTG CTG	2306
Glu Asp Ala Asp Ile Arg Gly Lys Gly Phe Asp Trp Pro Leu Leu	
600	
GTG AAG GAC TTC AAC CTG CTT CGC TGG CTT GGT GCC AAC GCT TTC	2351
Val Lys Asp Phe Asn Leu Leu Arg Trp Leu Gly Ala Asn Ala Phe	
610 620	
CGT ACC AGC CAC TAC CCC TAT GCA GAG GAA GTG ATG CAG ATG TGT	2396
Arg Thr Ser His Tyr Pro Tyr Ala Glu Glu Val Met Gln Met Cys	
630	
GAC CGC TAT GGG ATT GTG GTC ATC GAT GAG TGT CCC GGC GTG GGC	2441
Asp Arg Tyr Gly Ile Val Val Ile Asp Glu Cys Pro Gly Val Gly	
640 650	
CTG GCG CTG CCG CAG TTC TTC AAC AAC GTT TCT CTG CAT CAC CAC	2486
Leu Ala Leu Pro Gln Phe Phe Asn Asn Val Ser Leu His His His	
660	
ATG CAG GTG ATG GAA GAA GTG GTG CGT AGG GAC AAG AAC CAC CCC	2531
Met Gln Val Met Glu Glu Val Val Arg Arg Asp Lys Asn His Pro	
670 680	
GCG GTC GTG ATG TGG TCT GTG GCC AAC GAG CCT GCG TCC CAC CTA	2576
Ala Val Val Met Trp Ser Val Ala Asn Glu Pro Ala Ser His Leu	
690	
GAA TCT GCT GGC TAC TAC TTG AAG ATG GTG ATC GCT CAC ACC AAA	2621
Glu Ser Ala Gly Tyr Tyr Leu Lys Met Val Ile Ala His Thr Lys	
700 710	
TCC TTG GAC CCC TCC CGG CCT GTG ACC TTT GTG AGC AAC TCT AAC	2666
Ser Leu Asp Pro Ser Arg Pro Val Thr Phe Val Ser Asn Ser Asn	
720	
TAT GCA GCA GAC AAG GGG GCT CCG TAT GTG GAT GTG ATC TGT TTG	2711
Tyr Ala Ala Asp Lys Gly Ala Pro Tyr Val Asp Val Ile Cys Leu	
730 740	
AAC AGC TAC TAC TCT TGG TAT CAC GAC TAC GGG CAC CTG GAG TTG	2756
Asn Ser Tyr Tyr Ser Trp Tyr His Asp Tyr Gly His Leu Glu Leu	
750	
ATT CAG CTG CAG CTG GCC ACC CAG TTT GAG AAC TGG TAT AAG AAG	2801
Ile Gln Leu Gln Leu Ala Thr Gln Phe Glu Asn Trp Tyr Lys Lys	
760 770	
TAT CAG AAG CCC ATT ATT CAG AGC GAG TAT GGA GCA GAA ACG ATT	2846
Tyr Gln Lys Pro Ile Ile Gln Ser Glu Tyr Gly Ala Glu Thr Ile	
780	
GCA GGG TTT CAC CAG GAT CCA CCT CTG ATG TTC ACT GAA GAG TAC	2891

Ala	Gly	Phe	His	Gln	Asp	Pro	Pro	Leu	Met	Phe	Thr	Glu	Glu	Tyr		
				790										800		
CAG	AAA	AGT	CTG	CTA	GAG	CAG	TAC	CAT	CTG	GGT	CTG	GAT	CAA	AAA		2936
Gln	Lys	Ser	Leu	Leu	Glu	Gln	Tyr	His	Leu	Gly	Leu	Asp	Gln	Lys		
								810								
CGC	AGA	AAA	TAT	GTG	GTT	GGA	GAG	CTC	ATT	TGG	AAT	TTT	GCC	GAT		2981
Arg	Arg	Lys	Tyr	Val	Val	Gly	Glu	Leu	Ile	Trp	Asn	Phe	Ala	Asp		
				820										830		
TTC	ATG	ACT	GAA	CAG	TCA	CCG	ACG	AGA	GTG	CTG	GGG	ATT	AAA	AAG		3026
Phe	Met	Thr	Glu	Gln	Ser	Pro	Thr	Arg	Val	Leu	Gly	Asn	Lys	Lys		
								840								
GGG	ATC	TTC	ACT	CGG	CAG	AGA	CAA	CCA	AAA	AGT	GCA	GCG	TTC	CTT		3071
Gly	Ile	Phe	Thr	Arg	Gln	Arg	Gln	Pro	Lys	Ser	Ala	Ala	Phe	Leu		
				850										860		
TTG	CGA	GAG	AGA	TAC	TGG	AAG	ATT	GCC	AAT	GAA	ACC	AGG	TAT	CCC		3116
Leu	Arg	Glu	Arg	Tyr	Trp	Lys	Ile	Ala	Asn	Glu	Thr	Arg	Tyr	Pro		
								870								
CAC	TCA	GTA	GCC	AAG	TCA	CAA	TGT	TTG	GAA	AAC	AGC	CCG	TTT	ACT		3161
His	Ser	Val	Ala	Lys	Ser	Gln	Cys	Leu	Glu	Asn	Ser	Pro	Phe	Thr		
				880										890		
TGA	GCA	A	G	A	C	T	G	A	T	A	C	T	G	C		3214
TCC	A	C	A	G	C	A	G	C	A	G	T	G	C	T	C	3264
CGT	T	T	C	T	G	G	C	T	T	T	T	G	T	G	G	3314.

17. (Withdrawn) A vector containing a nucleic acid as claimed in claim 14.
18. (Withdrawn) A host cell containing a nucleic acid as claimed in claim 14 or a vector as claimed in claim 17.
19. (Withdrawn) A host cell as claimed in claim 18, which is a BHK, CHO, COS, HeLa, insect, tobacco plant, yeast or *E. coli* cell.
20. (Withdrawn) A transgenic mammal with the exception of a human, containing a DNA as claimed in claim 14 or a vector as claimed in claim 17.
21. (Withdrawn) A process for preparing a compound as claimed in claim 1, which comprises
  - a) introducing a nucleic acid as claimed in claim 14 or a vector as claimed in claim 17 into a host cell,
  - b) cultivating the host cell, and

c) isolating the compound.

22. (Withdrawn) A process for preparing a compound as claimed in claim 1, which comprises

a) cultivating a host cell as claimed in claim 18, and

b) isolating the compound.

23. (Canceled).

24. (Canceled).

25. (Previously Presented) A pharmaceutical composition comprising a compound as claimed in claim 1 and a physiologically acceptable carrier.

26. (Previously Presented) A diagnostic aid comprising a compound as claimed in claim 1.

27. (Previously Presented) A compound as claimed in claim 6, wherein the lactamase enzyme is a *Bacillus cereus*  $\beta$ -lactamase II.

28. (Previously Presented) A compound as claimed in claim 6, wherein the carboxypeptidase enzyme is a carboxypeptidase G2 from *Pseudomonas*.

29. (Previously Presented) A compound as claimed in claim 10, which has undergone secretory expression in *Hansenula polymorpha*.

30. (Currently Amended) A compound as claimed in claim 1, wherein at ~~least~~ least one antigen binding region and at least one prodrug-activating enzyme form an sFv- $\beta$ -lactamase fusion protein.

31. (Previously Presented) A compound as claimed in claim 11, wherein the chemical glycosylation involves at least one of galactosylation or mannosylation.



32. (Previously Presented) A compound as claimed in claim 12, wherein the chemical glycosylation involves at least one of galactosylation or mannosylation.

33. (Previously Presented) A method of treating cancer comprising administering a compound claimed in claim 1 to a host in need thereof and subsequently administering a prodrug to be activated by the enzyme portion of the compound of claim 1.

34. (Currently Amended) A compound comprising one or more antigen binding regions linked to at least one prodrug-activating enzyme, wherein

- a) the antigen binding regions consist of a single polypeptide chain;
- b) the single polypeptide chain is comprised of a first variable domain, a second variable domain, and a polypeptide linker connecting the first variable domain and the second variable domain, wherein a nucleotide sequence encoding the polypeptide linker is formed by two partially overlapping PCR primers during a PCR reaction that links the first variable domain and the second variable domain; ~~and~~ wherein
- c) the compound has a monovalent, bivalent, or multivalent structure; and wherein
- d) the compound is glycosylated.